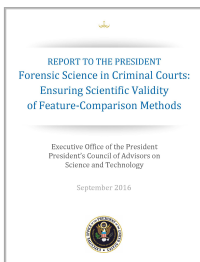


PCAST report



- DNA mixture limits
3 contributors
20% fraction
- Bitemark
- Firearm
- Footwear
- Hair



Transparency in DNA Evidence

President's Council of Advisors
on Science and Technology
November, 2016
Washington, DC

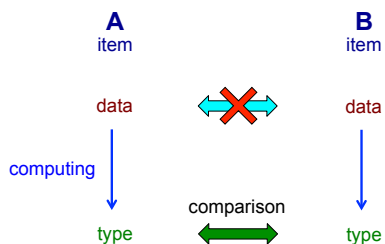
Mark W Perlin, PhD, MD, PhD
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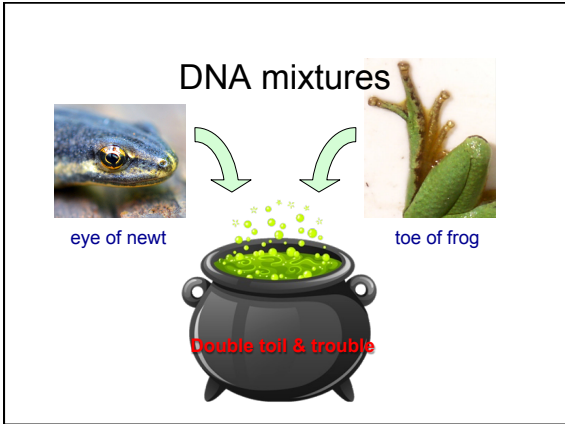


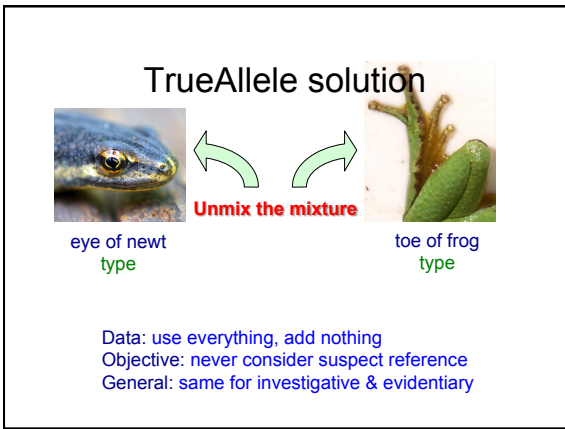
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Pattern evidence







Validation studies

JOURNAL OF FORENSIC SCIENCES

FORENSIC SCIENCES

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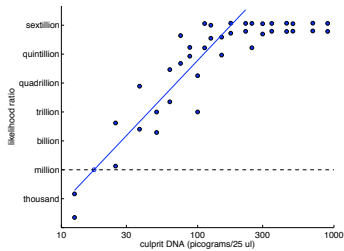
Mark W. Perlin,¹ Ph.D., M.D.; Jennifer M. Hornyak,¹ M.S.; Garrett Sugimoto,² M.S.; and Kevin W.P. Miller,² Ph.D.

TrueAllele® Genotype Identification on DNA Mixtures Containing up to Five Unknown Contributors*

ABSTRACT: Computer methods have been developed for mathematically interpreting mixed and low-template DNA. The genotype modeling approach computationally separates out the contributors to a mixture, with uncertainty measured through probability. Collections of inbred genotypes calculate a likelihood ratio (LR) which measures identification information. This study statistically examined the genotype modeling performance of Cybernetic TrueAllele® computer system. High- and low-template DNA mixtures of known contributor compositions containing 2, 3, 4, and 5 contributors were tested. Sensitivity, specificity, and reproducibility were established through LR quantification in each of these eight groups. Coverage analysis tested LR behavior as it related to mixture to DNA amount or contributor number. Analysis of variance found that consistent solutions were produced, since a sufficient number of contributors were considered. This study demonstrates the stability of TrueAllele operations on complex DNA mixtures of representative forensic composition. The results can help predict an alternative outcome for a DNA mixture analysis.

KEYWORDS: forensic science; DNA mixtures; genotype modeling; validation study; likelihood ratio; probabilistic; genotyping

Linear relationship



Inclusion probability

2005 NIST study

Some Differences in Reporting Statistics		Cases		
LabID	Kits Used	Caucasians	African-Americans	Hispanics
90	ProPlus/Cofiler	1.18E+15	2.13E+14	3.08E+15
34	ProPlus/Cofiler	2.40E+11	7.86E+09	9.90E+10
33	ProPlus/Cofiler	2.94E+09	1.12E+08	1.74E+09
6	ProPlus/Cofiler	40,000,000	3,500,000	280,000,000
9	ProPlus/Cofiler	1.14E+07	1.97E+07	1.54E+08
79	ProPlus/Cofiler	390,000	4.99E+05	1,350,000
16	ProPlus/Cofiler	434,600	31,710	399,100

Remember that these labs are interpreting the same MIX05 electropherograms

When not "inconclusive":

213 trillion (14)

31 thousand (4)

Government failure



NIST
National Institute of
Standards and Technology
U.S. Department of Commerce

Random counting



Research Article
Inclusion probability for DNA mixtures is a subjective one-sided match statistic unrelated to identification information

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Peer review

Funding sources for articles listed on Dr. Eric Lander's website
https://biology.mit.edu/people/eric_lander#selected_publications

Genome of the marsupial *Monodelphis domestica* reveals innovation in non-coding sequences

Generation of the *Monodelphis domestica* sequence at the Broad Institute of MIT and Harvard was supported by grants from the National Human Genome Research Institute (NHGRI).

For work from other members of the Opossum Genome Sequencing Consortium, we acknowledge the support of the National Institutes of Health (NHGRI, NIAID, NLM), the National Science Foundation,

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Telemedicine and Advanced Technology Research Center TATRC/DOD,

the UK Medical Research Council and the Australian Research Council.

Justice



Transparency

- open crime lab data to outside scrutiny
- open CODIS database to everyone
- DNA mixtures solved ten years ago
- no more money for failed government
- replace bad government with good science

PCAST agenda

Wasteful NIST validation study
Impact on justice & injustice

- Give NIST & FBI tens of millions of dollars
- Concentrate forensic power at NIST
- Delegitimize established forensic science
- Undermine reliable DNA evidence
In Indiana: Forest, Wade, Pinkins

In Washington: **the problem is the solution**

Arbitrary nonscientific limits

DNA mixture limits
3 contributors ?
20% fraction

NIST recommended limits to PCAST
NIST benefits financially from limits
NIST benefits politically from limits

- Conflict with Daubert factors: testing, error rate, peer-review & general acceptance
- Disconnected from papers cited by PCAST
- Jeopardize every DNA crime lab process
- If best DNA goes, all forensic evidence goes

What you can do



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